

SEQUENCE LISTING

<110> WALLACH, David
KOVALENKO, Andrei

<120> MODULATORS OF THE FUNCTION OF RECEPTORS OF THE TNG/NGF RECEPTOR FAMILY AND OTHER PROTEINS

<130> WALLACH=22A

<140> NOT YET ASSIGNED

<141> 2001-08-13

<150> PCT/IL98/00125

<151> 1998-03-19

<150> IL 120485

<151> 1997-03-19

<150> 09/381,358

<151> 1999-09-20

<160> 2

<170> PatentIn version 3.0

<210> 1

<211> 2119

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (217)..(1782)

<400> 1

tagggagacc caagcttctc gacggccatt accaatcgcg aaaccggcag ggcggccact 60

gtggcggggc tctttccccc tttcgccctca gctaccctc agctccgcta gtcgccagtc 120

cgggggtcgtc gccggttggg gcgggagctg ctcgcccccg ccgccgtccc cgtcgccgct 180

tccgggtcca ggccccctcg gccgcctgcc gccgtc atg agg ctg cgg gtg cgg 234
Met Arg Leu Arg Val Arg
1 5

ctt ctg aag cgg acc tgg ccg ctg gag gtg ccc gag acg gag ccg acg 282
Leu Leu Lys Arg Thr Trp Pro Leu Glu Val Pro Glu Thr Glu Pro Thr
10 15 20

ctg ggg cat ttg cgc tcg cac ctg agg ctg tcc ctg ctg tgc acc tgg 330
Leu Gly His Leu Arg Ser His Leu Arg Leu Ser Leu Leu Cys Thr Trp
25 30 35

ggg tac agt tct aat acc cga ttt aca att aca ttg aac tac aag gat 378
Gly Tyr Ser Ser Asn Thr Arg Phe Thr Ile Thr Leu Asn Tyr Lys Asp
40 45 50

ccc ctc act gga gat gaa gag acc ttg gct tca tat ggg att gtt tct 426
Pro Leu Thr Gly Asp Glu Glu Thr Leu Ala Ser Tyr Gly Ile Val Ser
55 60 65 70

ggg gac ttg ata tgt ttg att ctt caa gat gac att cca gcg cct aat 474

Gly	Asp	Leu	Ile	Cys	Leu	Ile	Leu	Gln	Asp	Asp	Ile	Pro	Ala	Pro	Asn		
				75					80					85			
ata	cct	tca	tcc	aca	gat	tca	gag	cat	tct	tca	ctc	cag	aat	aat	gag	522	
Ile	Pro	Ser	Ser	Thr	Asp	Ser	Glu	His	Ser	Ser	Leu	Gln	Asn	Asn	Glu		
			90					95					100				
caa	ccc	tct	ttg	gcc	acc	agc	tcc	aat	cag	act	agc	atg	cag	gat	gaa	570	
Gln	Pro	Ser	Leu	Ala	Thr	Ser	Ser	Asn	Gln	Thr	Ser	Met	Gln	Asp	Glu		
		105					110					115					
caa	cca	agt	gat	tca	ttc	caa	gga	cag	gca	gcc	cag	tct	ggg	gtt	tgg	618	
Gln	Pro	Ser	Asp	Ser	Phe	Gln	Gly	Gln	Ala	Ala	Gln	Ser	Gly	Val	Trp		
		120				125					130						
aat	gac	gac	agt	atg	tta	ggg	cct	agt	caa	aat	ttt	gaa	gct	gag	tca	666	
Asn	Asp	Asp	Ser	Met	Leu	Gly	Pro	Ser	Gln	Asn	Phe	Glu	Ala	Glu	Ser		
135					140					145					150		
att	caa	gat	aat	gcg	cat	atg	gca	gag	ggc	aca	ggg	ttc	tat	ccc	tca	714	
Ile	Gln	Asp	Asn	Ala	His	Met	Ala	Glu	Gly	Thr	Gly	Phe	Tyr	Pro	Ser		
				155					160					165			
gaa	ccc	atg	ctc	tgt	agt	gaa	tcg	gtg	gaa	ggg	caa	gtg	cca	cat	tca	762	
Glu	Pro	Met	Leu	Cys	Ser	Glu	Ser	Val	Glu	Gly	Gln	Val	Pro	His	Ser		
			170					175					180				
tta	gag	acc	ttg	tat	caa	tca	gct	gac	tgt	tct	gat	gcc	aat	gat	gcc	810	
Leu	Glu	Thr	Leu	Tyr	Gln	Ser	Ala	Asp	Cys	Ser	Asp	Ala	Asn	Asp	Ala		
		185					190					195					
ttg	ata	gtg	ttg	ata	cat	ctt	ctc	atg	ttg	gag	tca	ggg	tac	ata	cct	858	
Leu	Ile	Val	Leu	Ile	His	Leu	Leu	Met	Leu	Glu	Ser	Gly	Tyr	Ile	Pro		
		200				205					210						
cag	ggc	acc	gaa	gcc	aaa	gca	ctg	tcc	atg	ccg	gag	aag	tgg	aag	ttg	906	
Gln	Gly	Thr	Glu	Ala	Lys	Ala	Leu	Ser	Met	Pro	Glu	Lys	Trp	Lys	Leu		
215					220					225					230		
agc	ggg	gtg	tat	aag	ctg	cag	tac	atg	cat	cct	ctc	tgc	gag	ggc	agc	954	
Ser	Gly	Val	Tyr	Lys	Leu	Gln	Tyr	Met	His	Pro	Leu	Cys	Glu	Gly	Ser		
				235					240					245			
tcc	gct	act	ctc	acc	tgt	gtg	cct	ttg	gga	aac	ctg	att	gtt	gta	aat	1002	
Ser	Ala	Thr	Leu	Thr	Cys	Val	Pro	Leu	Gly	Asn	Leu	Ile	Val	Val	Asn		
			250					255					260				
gct	aca	cta	aaa	atc	aac	aat	gag	att	aga	agt	gtg	aaa	aga	ttg	cag	1050	
Ala	Thr	Leu	Lys	Ile	Asn	Asn	Glu	Ile	Arg	Ser	Val	Lys	Arg	Leu	Gln		
		265					270					275					
ctg	cta	cca	gaa	tct	ttt	att	tgc	aaa	gag	aaa	cta	ggg	gaa	aat	gta	1098	
Leu	Leu	Pro	Glu	Ser	Phe	Ile	Cys	Lys	Glu	Lys	Leu	Gly	Glu	Asn	Val		
		280				285					290						
gcc	aac	ata	tac	aaa	gat	ctt	cag	aaa	ctc	tct	cgc	ctc	ttt	aaa	gac	1146	
Ala	Asn	Ile	Tyr	Lys	Asp	Leu	Gln	Lys	Leu	Ser	Arg	Leu	Phe	Lys	Asp		
295					300					305					310		
cag	ctg	gtg	tat	cct	ctt	ctg	gct	ttt	acc	cga	caa	gca	ctg	aac	cta	1194	
Gln	Leu	Val	Tyr	Pro	Leu	Leu	Ala	Phe	Thr	Arg	Gln	Ala	Leu	Asn	Leu		
				315					320					325			

```

cca gat gta ttt ggg ttg gtc gtc ctc cca ttg gaa ctg aaa cta cgg      1242
Pro Asp Val Phe Gly Leu Val Val Leu Pro Leu Glu Leu Lys Leu Arg
330 335 340

atc ttc cga ctt ctg gat gtt cgt tcc gtc ttg tct ttg tct gcg gtt      1290
Ile Phe Arg Leu Leu Asp Val Arg Ser Val Leu Ser Leu Ser Ala Val
345 350 355

tgt cgt gac ctc ttt act gct tca aat gac cca ctc ctg tgg agg ttt      1338
Cys Arg Asp Leu Phe Thr Ala Ser Asn Asp Pro Leu Leu Trp Arg Phe
360 365 370

tta tat ctg cgt gat ttt cga gac aat act gtc aga gtt caa gac aca      1386
Leu Tyr Leu Arg Asp Phe Arg Asp Asn Thr Val Arg Val Gln Asp Thr
375 380 385 390

gat tgg aaa gaa ctg tac agg aag agg cac ata caa aga aaa gaa tcc      1434
Asp Trp Lys Glu Leu Tyr Arg Lys Arg His Ile Gln Arg Lys Glu Ser
395 400 405

ccg aaa ggg cgg ttt gtg atg ctc ctg cca tcg tca act cac acc att      1482
Pro Lys Gly Arg Phe Val Met Leu Leu Pro Ser Ser Thr His Thr Ile
410 415 420

cca ttc tat ccc aac ccc ttg cac cct agg cca ttt cct agc tcc cgc      1530
Pro Phe Tyr Pro Asn Pro Leu His Pro Arg Pro Phe Pro Ser Ser Arg
425 430 435

ctt cct cca gga att atc ggg ggt gaa tat gac caa aga cca aca ctt      1578
Leu Pro Pro Gly Ile Ile Gly Gly Glu Tyr Asp Gln Arg Pro Thr Leu
440 445 450

ccc tat gtt gga gac cca atc agt tca ctc att cct ggt cct ggg gag      1626
Pro Tyr Val Gly Asp Pro Ile Ser Ser Leu Ile Pro Gly Pro Gly Glu
455 460 465 470

acg ccc agc cag ttt cct cca ctg aga cca cgc ttt gat cca gtt ggc      1674
Thr Pro Ser Gln Phe Pro Pro Leu Arg Pro Arg Phe Asp Pro Val Gly
475 480 485

cca ctt cca gga cct aac ccc atc ttg cca ggg cga ggc ggc ccc aat      1722
Pro Leu Pro Gly Pro Asn Pro Ile Leu Pro Gly Arg Gly Gly Pro Asn
490 495 500

gac aga ttt ccc ttt aga ccc agc agg ggt cgg cca act gat ggc cgg      1770
Asp Arg Phe Pro Phe Arg Pro Ser Arg Gly Arg Pro Thr Asp Gly Arg
505 510 515

ctg tca ttc atg tgattgattt gtaatttcatt ttctggagct ccatttgttt      1822
Leu Ser Phe Met
520

ttgtttctaa actacagatg tcaactcctt ggggtgctga tctcgagtgt tattttctga      1882

ttgtggtggt gagagttgca ctcccagaaa ccttttaaga gatacattta tagccctagg      1942

ggtggtatga cccaaagggt cctctgtgac aagggtggcc ttgggaatag ttggctgcc      2002

atctccctgc tcttggttct cctctagatt gaagtttggt ttctgatgct gttcttacca      2062

gattaaaaaa aagtgtaaat taaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaa      2119

```

<210> 2
 <211> 522
 <212> PRT
 <213> Homo sapiens

<400> 2

Met Arg Leu Arg Val Arg Leu Leu Lys Arg Thr Trp Pro Leu Glu Val
 1 5 10 15

Pro Glu Thr Glu Pro Thr Leu Gly His Leu Arg Ser His Leu Arg Leu
 20 25 30

Ser Leu Leu Cys Thr Trp Gly Tyr Ser Ser Asn Thr Arg Phe Thr Ile
 35 40 45

Thr Leu Asn Tyr Lys Asp Pro Leu Thr Gly Asp Glu Glu Thr Leu Ala
 50 55 60

Ser Tyr Gly Ile Val Ser Gly Asp Leu Ile Cys Leu Ile Leu Gln Asp
 65 70 75 80

Asp Ile Pro Ala Pro Asn Ile Pro Ser Ser Thr Asp Ser Glu His Ser
 85 90 95

Ser Leu Gln Asn Asn Glu Gln Pro Ser Leu Ala Thr Ser Ser Asn Gln
 100 105 110

Thr Ser Met Gln Asp Glu Gln Pro Ser Asp Ser Phe Gln Gly Gln Ala
 115 120 125

Ala Gln Ser Gly Val Trp Asn Asp Asp Ser Met Leu Gly Pro Ser Gln
 130 135 140

Asn Phe Glu Ala Glu Ser Ile Gln Asp Asn Ala His Met Ala Glu Gly
 145 150 155 160

Thr Gly Phe Tyr Pro Ser Glu Pro Met Leu Cys Ser Glu Ser Val Glu
 165 170 175

Gly Gln Val Pro His Ser Leu Glu Thr Leu Tyr Gln Ser Ala Asp Cys
 180 185 190

Ser Asp Ala Asn Asp Ala Leu Ile Val Leu Ile His Leu Leu Met Leu
 195 200 205

Glu Ser Gly Tyr Ile Pro Gln Gly Thr Glu Ala Lys Ala Leu Ser Met
 210 215 220

Pro Glu Lys Trp Lys Leu Ser Gly Val Tyr Lys Leu Gln Tyr Met His
225 230 235 240

Pro Leu Cys Glu Gly Ser Ser Ala Thr Leu Thr Cys Val Pro Leu Gly
245 250 255

Asn Leu Ile Val Val Asn Ala Thr Leu Lys Ile Asn Asn Glu Ile Arg
260 265 270

Ser Val Lys Arg Leu Gln Leu Leu Pro Glu Ser Phe Ile Cys Lys Glu
275 280 285

Lys Leu Gly Glu Asn Val Ala Asn Ile Tyr Lys Asp Leu Gln Lys Leu
290 295 300

Ser Arg Leu Phe Lys Asp Gln Leu Val Tyr Pro Leu Leu Ala Phe Thr
305 310 315 320

Arg Gln Ala Leu Asn Leu Pro Asp Val Phe Gly Leu Val Val Leu Pro
325 330 335

Leu Glu Leu Lys Leu Arg Ile Phe Arg Leu Leu Asp Val Arg Ser Val
340 345 350

Leu Ser Leu Ser Ala Val Cys Arg Asp Leu Phe Thr Ala Ser Asn Asp
355 360 365

Pro Leu Leu Trp Arg Phe Leu Tyr Leu Arg Asp Phe Arg Asp Asn Thr
370 375 380

Val Arg Val Gln Asp Thr Asp Trp Lys Glu Leu Tyr Arg Lys Arg His
385 390 395 400

Ile Gln Arg Lys Glu Ser Pro Lys Gly Arg Phe Val Met Leu Leu Pro
405 410 415

Ser Ser Thr His Thr Ile Pro Phe Tyr Pro Asn Pro Leu His Pro Arg
420 425 430

Pro Phe Pro Ser Ser Arg Leu Pro Pro Gly Ile Ile Gly Gly Glu Tyr
435 440 445

Asp Gln Arg Pro Thr Leu Pro Tyr Val Gly Asp Pro Ile Ser Ser Leu
450 455 460

Ile Pro Gly Pro Gly Glu Thr Pro Ser Gln Phe Pro Pro Leu Arg Pro
465 470 475 480

Gly Arg Gly Gly Pro Asn Asp Arg Phe Pro Phe Arg Pro Ser Arg Gly
500 505 510

Arg Pro Thr Asp Gly Arg Leu Ser Phe Met
515 520